



## SEQUENCE LISTING

RECEIVED

OCT 12 2001

TECH CENTER 1600/2900

<110> Buechler, Joe  
Valkirs, Gunars  
Gray, Jeff  
Lonberg, Nils  
Biosite Diagnostics, Inc.  
GenPharm International

<120> Human Antibodies

<130> 020015-000110US

<140> 09/453,234

<141> 1999-12-01

<150> US 60/157,415

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<210> 11

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<210> 20

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<210> 22

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<223> Description of Artificial Sequence: Primer 5

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<223> Description of Artificial Sequence: Primer 970

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<210> 31

<211> 47

<212> DNA

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<223> Description of Artificial Sequence: Example 19  
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tgatgtgaat tctcagccct cttcaa 86

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<223> Description of Artificial Sequence: Example 19  
Primer C

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<210> 34  
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<223> Description of Artificial Sequence: Example 19  
 Primer D

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 ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180  
 aggttcagtg gcagtggggc tgggacagac ttcactctca ccatcagcag cctagagcct 240  
 gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctcggac gttcggccaa 300  
 gggaccaagg tggaaatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcga 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
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<210> 36  
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 <212> PRT  
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<400> 36

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100					105					110						
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
115					120					125						
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	
130					135					140						
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	
145					150					155					160	
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	
165					170					175						
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	
180					185					190						
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	
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Phe	Asn	Arg	Gly	Glu	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	
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Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc															96	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	
			20					25					30			
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc															144	
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	
		35					40					45				
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt															192	
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	
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ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag															240	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	
65					70					75					80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct															288	



Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro	
				85					90					95		
Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Thr	Val	
				100					105					110		
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	
				115					120					125		
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
				130					135					140		
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	
				145					150					155		
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	
				165					170					175		
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	
				180					185					190		
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	
				195					200					205		
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	
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Ala	Ser															
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1				5					10					15			
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc																	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser		
			20					25					30				
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc cac																	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	His		
		35					40					45					
atc tat ggt gca tcc aga agg gcc act ggc atc cca gac agg ttc agt																	192
Ile	Tyr	Gly	Ala	Ser	Arg	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser		
	50					55				60							

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 cct gaa gat ttt gca gtg tat tac tgt cag cag ttt ggt agc tca ttc 288  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Phe  
 85 90 95  
 act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205  
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 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
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 35 40 45  
 Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Phe  
 85 90 95  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
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 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30  
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

ata ttc act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg 336
Ile Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
100 105 110

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95  
 Ile Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val  
 100 105 110  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
 115 120 125  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 130 135 140  
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 145 150 155 160  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 165 170 175  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 180 185 190  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
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 Ala Ser  
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 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc acc 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr  
 20 25 30  
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35	40	45	
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60			192
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80			240
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca ttc Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe 85 90 95			288
act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala 100 105 110			336
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125			384
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140			432
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160			480
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175			528
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185 190			576
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 205			624
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc Phe Asn Arg Gly Glu Ser Tyr Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 210 215 220			672

&lt;210&gt; 44

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-8L

&lt;400&gt; 44

Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5				10						15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Thr
		20						25				30			

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60		
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80		
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe 85 90 95		
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala 100 105 110		
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125		
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140		
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160		
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175		
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185 190		
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 205		
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 210 215 220		

<210> 45  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-10L

<220>  
 <221> CDS  
 <222> (1) .. (672)

<400> 45	
gat gtt gtg atg aca cag tct cca gcc acc ctg tct ttg tct cca ggg Asp Val Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 1 5 10 15	48
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr 20 25 30	96
tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 40 45	144

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192  
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccc 288  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
 85 90 95

act ttc ggc gga ggg acc aag gtg gag atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 210 215 220

&lt;210&gt; 46

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-10L

&lt;400&gt; 46

Asp Val Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 210 215 220

<210> 47  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-21L

<220>  
 <221> CDS  
 <222> (1)..(672)

<400> 47  
 gcc atc cgg atg acc cag tct cca tcc ttc ctg tct gca tct gta gga 48  
 Ala Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tat 96  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
 20 25 30  
 tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc 144  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt gtc 192  
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Val  
 50 55 60  
 agt gga tct ggg aca gat ctc act ctc acc atc agc agt ctg caa cct 240  
 Ser Gly Ser Gly Thr Asp Leu Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 gaa gat ttt gca act tat tac tgt cag tgt ggt tac agt aca cca ttc 288  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Tyr Ser Thr Pro Phe  
 85 90 95  
 act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205  
 ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 210 215 220

&lt;210&gt; 48

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-21L

&lt;400&gt; 48

Ala Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Val  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Leu Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Tyr Ser Thr Pro Phe  
 85 90 95  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
 210 215 220

<210> 49  
 <211> 678  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-23L

<220>  
 <221> CDS  
 <222> (1)..(678)

<400> 49  
 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30  
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser		
50						55					60						
ggc	agt	ggg	tct	ggg	aca	gac	ttc	act	ctc	acc	atc	agc	aga	ctg	gag	240	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu		
65					70					75					80		
cct	gaa	gat	ttt	gca	gtg	tat	tac	tgt	cag	cag	tat	ggg	agc	tca	cct	288	
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro		
				85					90					95			
ccg	tac	act	ttt	ggc	cag	ggg	acc	aag	ctg	gag	atc	aaa	cga	act	gtg	336	
Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val		
			100					105					110				
gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	384	
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys		
			115				120					125					
tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	aga	432	
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg		
	130					135					140						
gag	gcc	aaa	gta	cag	tgg	agg	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	aac	480	
Glu	Ala	Lys	Val	Gln	Trp	Arg	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn		
145				150					155					160			
tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	agc	528	
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser		
				165					170					175			
ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	aaa	576	
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys		
			180					185					190				
gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	624	
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr		
			195				200						205				
aag	agc	ttc	aac	agg	gga	gag	tct	tat	cca	tat	gat	gtg	cca	gat	tat	672	
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr		
	210					215					220						
gcg	agc															678	
Ala	Ser																
225																	

<210> 50  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens  
 <223> M1-23L

<400> 50  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
           35                          40                          45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
           50                          55                          60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
           65                          70                          75                          80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
                           85                          90                          95  
 Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val  
                           100                          105                          110  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
           115                          120                          125  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
           130                          135                          140  
 Glu Ala Lys Val Gln Trp Arg Val Asp Asn Ala Leu Gln Ser Gly Asn  
           145                          150                          155                          160  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
                           165                          170                          175  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                           180                          185                          190  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
           195                          200                          205  
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
           210                          215                          220  
 Ala Ser  
 225

<210> 51

<211> 672

<212> DNA

<213> Homo sapiens

<220>

<223> M1-25L

<400> 51

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 aacagggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcattcac ttccggccct 300  
 gggaccaaag tggatatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcga 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccacaggggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac agggggagagt cttatccata tgatgtgcc 660

gattatgcga gc

672

<210> 52  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> M1-25L

<400> 52  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
   1                  5                  10                  15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
                   20                  25                  30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
           35                  40                  45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asn Arg Phe Ser  
       50                  55                  60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
   65                  70                  75                  80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe  
                   85                  90                  95  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
                   100                  105                  110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
           115                  120                  125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
       130                  135                  140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
   145                  150                  155                  160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
           165                  170                  175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
           180                  185                  190  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
       195                  200                  205  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Asn  
       210                  215                  220

<210> 53  
 <211> 675  
 <212> DNA

<213> Homo sapiens

<220>

<223> M1-1H

<220>

<221> CDS

<222> (1)..(675)

<400> 53

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	aag	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys	
1				5					10					15		
tcc	ctg	aga	ctc	tcc	tgt	gca	gcg	tct	gaa	ttc	acc	atc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Glu	Phe	Thr	Ile	Ser	Tyr	Tyr	
			20					25					30			
ggc	atg	cac	tgg	gtc	cgc	cag	gtt	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
gca	gct	gtc	tgg	tat	gat	gaa	agt	act	aca	tat	tct	cca	gac	tcc	gtg	192
Ala	Ala	Val	Trp	Tyr	Asp	Glu	Ser	Thr	Thr	Tyr	Ser	Pro	Asp	Ser	Val	
		50					55				60					
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	gat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75				80		
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
gcg	aga	gat	agg	gtg	ggc	ctc	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Arg	Val	Gly	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
			100					105					110			
gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
		115					120					125				
gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
	130					135					140					
ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145					150					155				160		
ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	528
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
				165				170					175			
tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	576
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
		180						185				190				
ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	624
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
		195					200					205				

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

cac 675  
 His  
 225

<210> 54  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M1-1H

<400> 54  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Ile Ser Tyr Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Ala Val Trp Tyr Asp Glu Ser Thr Thr Tyr Ser Pro Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 55  
 <211> 677  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-3H

<220>  
 <221> CDS  
 <222> (3)..(677)

<400> 55

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cc gat gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg      47
   Asp Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly
      1              5              10              15

agg tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac      95
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr
              20              25              30

tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg      143
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

gtg aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc      191
Val Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser
              50              55              60

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg      239
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
              65              70              75

tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac      287
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
              80              85              90              95

tgt gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc      335
Cys Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
              100              105              110

ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc      383
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
              115              120              125

ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc      431
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
              130              135              140

tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac      479
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
              145              150              155

tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag      527
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
              160              165              170              175

tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc      575
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Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser  
 180 185 190

agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc 623  
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
 195 200 205

aac acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac 671  
 Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His  
 210 215 220

cat cac 677  
 His His  
 225

<210> 56  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M1-3H

<400> 56  
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 57  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-4H

<220>  
 <221> CDS  
 <222> (1) .. (675)

<400> 57  
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 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30  
 ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192  
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val  
 50 55 60  
 aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336  
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140  
 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                   165                                  170                                  175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                   180                                  185                                  190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                   195                                  200                                  205

acc aag gtg gac aag aaa gca ggg ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Gly Pro Lys Ser His His His His His  
                   210                                  215                                  220

cac 675  
 His  
 225

<210> 58  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M1-4H

<400> 58  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
   1                                  5                                  10                                  15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
                   20                                  25                                  30  
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45  
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val  
                   50                                  55                                  60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95  
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                   100                                  105                                  110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
                   115                                  120                                  125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
                   130                                  135                                  140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
   145                                  150                                  155                                  160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                   165                                  170                                  175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Lys Ala Gly Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 59  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-5H

<220>  
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 <222> (1)..(675)

<400> 59  
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 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30  
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192  
 Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336  
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

cac 675  
 His  
 225

<210> 60  
 <211> 225  
 <212> PRT  
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 <223> M1-5H

<400> 60  
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
210 215 220

His  
225

<210> 61  
<211> 675  
<212> DNA  
<213> Homo sapiens

<220>  
<223> M1-8H

<220>  
<221> CDS  
<222> (1)..(675)

<400> 61  
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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
1 5 10 15  
tcc ctg aaa ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat 96  
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
20 25 30  
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
gca gct gta tgg tat gat gga agt aac aca tac tct cca gac tcc gtg 192  
Ala Ala Val Trp Tyr Asp Gly Ser Asn Thr Tyr Ser Pro Asp Ser Val  
50 55 60  
aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg gtg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr  
65 70 75 80  
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336  
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

cac 675  
 His  
 225

<210> 62

<211> 225

<212> PRT

<213> Homo sapiens

<223> M1-8H

<400> 62

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Ala Val Trp Tyr Asp Gly Ser Asn Thr Tyr Ser Pro Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
210 215 220

His  
225

<210> 63  
<211> 708  
<212> DNA  
<213> Homo sapiens

<220>  
<223> M1-10H

<220>  
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<222> (1) .. (708)

<400> 63  
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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gaa ggc tct gga ttc atc ttc agg aac cat 96  
Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His  
20 25 30  
cct ata cac tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca gtt agt ggt att ggt ggt gac aca tac tat gca gac tcc gtg aag 192  
Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc tcc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
                                     85                                    90                                    95

aga gaa tat tac tat ggt tgc ggg agt tat cgc gtt gac tac tac tac 336  
 Arg Glu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr  
                                     100                                    105                                    110

tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca 384  
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
                                     115                                    120                                    125

gcc tcc acc aag ggc cca tgc gtc ttc ccc ctg gca ccc tcc tcc aag 432  
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
                                     130                                    135                                    140

agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac 480  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
                                     145                                    150                                    155                                    160

ttc ccc gaa ccg gtg acg gtg tgc tgg aac tca ggc gcc ctg acc agc 528  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
                                     165                                    170                                    175

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc 576  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
                                     180                                    185                                    190

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc 624  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
                                     195                                    200                                    205

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag 672  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
                                     210                                    215                                    220

aaa gca gag ccc aaa tct cat cac cat cac cat cac 708  
 Lys Ala Glu Pro Lys Ser His His His His His His  
                                     225                                    230                                    235

&lt;210&gt; 64

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-10H

&lt;400&gt; 64

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
   1                                    5                                    10                                    15

Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His  
                                     20                                    25                                    30

Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                                     35                                    40                                    45

Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys  
                                     50                                    55                                    60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
   65                                    70                                    75                                    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr  
100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
130 135 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
145 150 155 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
165 170 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
180 185 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
195 200 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
210 215 220

Lys Ala Glu Pro Lys Ser His His His His His His  
225 230 235

<210> 65

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<223> M1-21H

<220>

<221> CDS

<222> (1)..(675)

<400> 65

cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg aag 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
20 25 30

ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192  
Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg agc agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg	336
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

&lt;210&gt; 66

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-21H

&lt;400&gt; 66

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
20 25 30

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
210 215 220

His  
225

<210> 67  
<211> 675  
<212> DNA  
<213> Homo sapiens

<220>  
<223> M1-23H

<220>  
<221> CDS  
<222> (1) .. (675)

<400> 67  
cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg agg 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt aac tat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
gca	gct	ata	tgg	tat	gat	gga	agt	aaa	aca	tac	aat	gca	gac	tcc	gtg	192	
Ala	Ala	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Thr	Tyr	Asn	Ala	Asp	Ser	Val		
	50					55					60						
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctg	tat	240	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
	65				70					75				80			
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85						90					95			
gcg	aga	gat	ggg	ata	ggc	tac	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336	
Ala	Arg	Asp	Gly	Ile	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu		
			100					105					110				
gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384	
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu		
		115					120					125					
gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432	
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys		
	130					135					140						
ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480	
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser		
	145				150					155				160			
ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	528	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser		
				165					170					175			
tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	576	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser		
			180					185					190				
ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	624	
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn		
		195					200					205					
acc	aag	gtg	gac	aag	aaa	gca	gag	ccc	aaa	tct	cat	cac	cat	cac	cat	672	
Thr	Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	His	His	His	His	His		
	210					215					220						
cac																675	
His																	
225																	

&lt;210&gt; 68

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-23H

&lt;400&gt; 68

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
                   20                                  25                                  30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45  
 Ala Ala Ile Trp Tyr Asp Gly Ser Lys Thr Tyr Asn Ala Asp Ser Val  
                   50                                  55                                  60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                                  70                                  75                                  80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                   85                                  90                                  95  
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                                   100                                  105                                  110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
                   115                                  120                                  125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
                   130                                  135                                  140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
                   145                                  150                                  155                                  160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                                   165                                  170                                  175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                                   180                                  185                                  190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                   195                                  200                                  205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
                   210                                  215                                  220  
 His  
 225

<210> 69  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> M1-25H

<220>  
 <221> CDS  
 <222> (1) .. (675)

<400> 69  
 cag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg 48  
 Gln Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
           1                                  5                                  10                                  15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr	
20 25 30	
ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg	144
Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
gca gct gtc tgg tat gat gga agt act aca tat cct cca gac tcc gtg	192
Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Pro Pro Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtt tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg	336
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

<210> 70  
 <211> 225  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M1-25H

&lt;400&gt; 70

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Pro Pro Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His

225

&lt;210&gt; 71

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(678)

&lt;220&gt;

&lt;223&gt; M2-11L

&lt;400&gt; 71

gaa ata gtg atg acg cag tct cca ggc acc ctg tct ttg tct cca ggg	48
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
gaa aga gcc acc ctg tcc tgc agg gcc agt cag ggt gtt agc agc agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg ctg	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctg acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
cca ttc act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg	336
Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val	
100 105 110	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aga	384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Arg	
115 120 125	
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctg caa tcg ggt aac	480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn	
145 150 155 160	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa	576
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys	
180 185 190	
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca	624
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr	
195 200 205	
aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat	672
Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr	
210 215 220	
gcg agc	678
Ala Ser	

225

<210> 72  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-11L

&lt;400&gt; 72

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val  
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Arg  
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
 210 215 220

Ala Ser  
 225

<210> 73  
 <211> 678  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(678)

<220>  
 <223> M2-12L

<400> 73

gaa ata gtg atg acg cag tct cca ggc acc ctg tct ttg tct cca ggg	48
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
gaa aga gcc acc ctc tcc tgc agg gcc agt cag ggt gtt agc agc agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
ccg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg	336
Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val	
100 105 110	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa	384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys	
115 120 125	
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac	480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn	
145 150 155 160	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa	576
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys	
180 185 190	
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca	624
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr	
195 200 205	

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672  
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
       210                      215                      220

gcg agc 678  
 Ala Ser  
 225

<210> 74  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-12L

<400> 74  
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
       1                      5                      10                      15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser  
           20                      25                      30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
           35                      40                      45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
       50                      55                      60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu  
       65                      70                      75                      80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
           85                      90                      95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val  
           100                      105                      110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
       115                      120                      125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
       130                      135                      140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
       145                      150                      155                      160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
           165                      170                      175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
           180                      185                      190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
       195                      200                      205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
       210                      215                      220

Ala Ser  
 225

<210> 75  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
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gaa aga gcc acc ctg tcc tgc agg gcc agt cag agt gtt agc agc agc 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg ctg 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

gtc agt ggg tct ggg aca gac ttc act ctg acc atc agc aga ctg gag 240  
 Val Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ttc 288  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe  
 85 90 95

act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctg caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctg agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

180										185					190										
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc																				624					
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser																									
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ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc																				672					
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	20										25					30									
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu																									
	35										40					45									
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser																									
	50										55					60									
Val Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu																									
	65										70					75					80				
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe																									
	85										90					95									
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala																									
	100										105					110									
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly																									
	115										120					125									
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala																									
	130										135					140									
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln																									
	145										150					155					160				
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser																									
	165										170					175									
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr																									
	180										185					190									
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser																									
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<220>  
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<220>  
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 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc acc 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr  
 20 25 30  
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca ttc 288  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe  
 85 90 95  
 act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

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ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc    672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
      210                      215                      220

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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Thr
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Val	Ser	Ser	Phe
				85					90					95	
Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Thr	Val	Ala	Ala
			100					105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145					150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
				165					170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
			180					185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser
	210					215					220				

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 <212> DNA  
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<220>  
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<400> 79

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tac ggt gca tcc agg agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ccc	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
atg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg	336
Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val	
100 105 110	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa	384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys	
115 120 125	
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac	480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn	
145 150 155 160	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa	576
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys	
180 185 190	

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
           195                                  200                                  205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672  
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
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gcg agc 678  
 Ala Ser  
 225

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                                   20                                  25                                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
                                   35                                  40                                  45

Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
           50                                  55                                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
           65                                  70                                  75                                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
                                   85                                  90                                  95

Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val  
                                   100                                  105                                  110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
                                   115                                  120                                  125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
           130                                  135                                  140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
           145                                  150                                  155                                  160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
                                   165                                  170                                  175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                                   180                                  185                                  190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
                                   195                                  200                                  205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
           210                                  215                                  220

Ala Ser  
225

<210> 81  
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<212> DNA  
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<220>  
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<222> (1)..(672)

<220>  
<223> M2-31L

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1 5 10 15  
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
20 25 30  
tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45  
tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192  
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60  
agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
65 70 75 80  
gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg 288  
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg  
85 90 95  
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca 336  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110  
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125  
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140  
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160  
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser

165										170					175					
agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	576				
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr					
			180					185					190							
gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	624				
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser					
		195					200					205								
ttc	aac	agg	gga	gag	tct	tat	cca	tat	gat	gtg	cca	gat	tat	gcg	agc	672				
Phe	Asn	Arg	Gly	Glu	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser					
	210					215					220									
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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Tyr					
		20					25					30								
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile					
	35					40						45								
Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly					
	50				55					60										
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro					
	65			70					75					80						
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Thr	Asn	Trp	Pro	Arg					
			85					90					95							
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala					
		100					105						110							
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly					
	115					120						125								
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala					
	130				135					140										
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln					
	145			150					155				160							
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser					
		165						170					175							
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr					
		180					185					190								
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser					
	195					200					205									

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
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<210> 83

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<212> DNA

<213> Homo sapiens

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<222> (1)..(672)

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<223> M2-32L

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr	
20 25 30	
tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc	144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile	
35 40 45	
tat gat gca tcc aac agg gcc gct ggc atc cca gcc agg ttc agt ggc	192
Tyr Asp Ala Ser Asn Arg Ala Ala Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	
agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	
gaa gat ttt gca gtt tat tac tgt cag caa cgt aac aac tgg cct ctc	288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Asn Trp Pro Leu	
85 90 95	
act ttc ggc gga ggg acc aag gtg gag atc aaa cga act gtg gct gca	336
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
                   180                  185                  190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
                   195                  200                  205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672  
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
                   210                  215                  220

<210> 84

<211> 224

<212> PRT

<213> Homo sapiens

<223> M2-32L

<400> 84

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
                   20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
                   35                  40                  45

Tyr Asp Ala Ser Asn Arg Ala Ala Gly Ile Pro Ala Arg Phe Ser Gly  
           50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
           65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Asn Trp Pro Leu  
                   85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
                   100                  105                  110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
           115                  120                  125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
           130                  135                  140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
           145                  150                  155                  160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
                   165                  170                  175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
           180                  185                  190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
           195                  200                  205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser

210

215

220

<210> 85  
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<220>  
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 <222> (1)..(678)

<220>  
 <223> M2-33L

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1 5 10 15	
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
ccg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg	336
Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val	
100 105 110	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa	384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys	
115 120 125	
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac	480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn	
145 150 155 160	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                   180                  185                  190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
                   195                  200                  205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672  
 Lys Ser Phe Asn Arg Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
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gcg agc 678  
 Ala Ser  
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                   20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
                   35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
           50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
           65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
                   85                  90                  95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val  
                   100                  105                  110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
                   115                  120                  125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
           130                  135                  140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
           145                  150                  155                  160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
                   165                  170                  175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                   180                  185                  190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr

195

200

205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr  
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Ala Ser  
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192  
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg 288  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg  
 85 90 95

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca 336  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145		150		155		160	
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc							528
Glu Ser Val Thr	Glu Gln Asp Ser Lys	Asp Ser Thr Tyr	Ser Leu Ser				
	165	170	175				
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac							576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr							
	180	185	190				
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc							624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser							
	195	200	205				
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc							672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser							
	210	215	220				

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 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
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<210> 89

<211> 672

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(672)

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<223> M2-35L

<400> 89

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1 5 10 15	
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr	
20 25 30	
tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc	144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile	
35 40 45	
tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc	192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	
agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	
gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg	288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg	
85 90 95	
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca	336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
                   165                                  170                                  175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
                   180                                  185                                  190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
                   195                                  200                                  205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672  
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                   210                                  215                                  220

<210> 90

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<212> PRT

<213> Homo sapiens

<223> M2-35L

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                   20                                  25                                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
                   35                                  40                                  45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
           50                                  55                                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
           65                                  70                                  75                                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg  
                   85                                  90                                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
                   100                                  105                                  110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
           115                                  120                                  125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
           130                                  135                                  140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
           145                                  150                                  155                                  160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
                   165                                  170                                  175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
                   180                                  185                                  190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
210 215 220

<210> 91

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(675)

<220>

<223> M2-11H

<400> 91

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Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
tcc	ctg	aga	ctc	tcc	tgt	gca	gcg	tct	gga	ttt	acc	ttc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Tyr	Tyr	
			20					25					30			
ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35				40						45				
aca	ctt	ata	acc	tat	gat	gga	gat	aat	aaa	tac	tat	gca	gac	tcc	gtg	192
Thr	Leu	Ile	Thr	Tyr	Asp	Gly	Asp	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
gcg	aga	gac	ggg	atc	ggg	tac	ttt	gac	tat	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Gly	Ile	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
			100					105					110			
gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
			115				120					125				
gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
	130					135					140					
ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145					150				155					160		

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                                   165                                  170                                  175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                                   180                                  185                                  190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                                   195                                  200                                  205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
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cac 675  
 His  
 225

<210> 92  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-11H

<400> 92  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
                                   20                                  25                                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                                   35                                  40                                  45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
                                   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                                   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                   85                                  90                                  95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                                   100                                  105                                  110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
                                   115                                  120                                  125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
                                   130                                  135                                  140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
                                   145                                  150                                  155                                  160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                                   165                                  170                                  175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                   180                                  185                                  190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                   195                                  200                                  205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
           210                                  215                                  220

His  
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<220>  
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tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
                                   20                                  25                                  30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gaa tgg atg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
                   35                                  40                                  45

aca ctt ata tcc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192  
 Thr Leu Ile Ser Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
           50                                  55                                  60

aag ggc cga ttc acc atc tcc aga gaa aat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr  
           65                                  70                                  75                                  80

ctg caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                   85                                  90                                  95

gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336  
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                   100                                  105                                  110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
           115                                  120                                  125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys

130	135	140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca			480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser			
145	150	155	160
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc			528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser			
	165	170	175
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc			576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser			
	180	185	190
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc agc			624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Ser			
	195	200	205
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat			672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His			
	210	215	220
cac			675
His			
225			
<210> 94			
<211> 225			
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<400> 94			
Asp Val Gln Leu Val Glu Ser Gly Gly Gly Val Val His Pro Gly Arg			
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr			
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met			
	35	40	45
Thr Leu Ile Ser Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val			
	50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr			
	65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
	100	105	110
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu			
	115	120	125
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys			
	130	135	140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Ser  
195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
210 215 220

His  
225

<210> 95  
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<212> DNA  
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<220>  
<223> M2-16H

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Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca gcg tct gga ttc agc ttg agt tac tat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Tyr Tyr  
20 25 30  
ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
gca gct gtc tgg tat gat gga agt act aga tat tct cca gac tcc gtg 192  
Ala Ala Val Trp Tyr Asp Gly Ser Thr Arg Tyr Ser Pro Asp Ser Val  
50 55 60  
aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336  
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140  
 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160  
 ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175  
 tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Thr Ser Leu Ser Ser Val Thr Val Pro Ser Ser Ser  
 180 185 190  
 ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205  
 acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220  
 cac 675  
 His  
 225

<210> 96  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-16H

<400> 96  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Tyr Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Arg Tyr Ser Pro Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 97  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (675)

<220>  
 <223> M2-18H

<400> 97  
 cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg aag 48  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc agc ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Tyr Tyr  
 20 25 30

ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192  
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val  
 50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

<400> 98

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Tyr	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Ala	Val	Trp	Tyr	Asp	Gly	Ser	Thr	Thr	Tyr	Ser	Pro	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                     85                    90                    95  
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                     100                    105                    110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
                     115                    120                    125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
                     130                    135                    140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
                     145                    150                    155                    160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                     165                    170                    175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                     180                    185                    190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                     195                    200                    205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
                     210                    215                    220  
 His  
 225

<210> 99  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(675)

<220>  
 <223> M2-20H

<400> 99  
 cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg agg 48  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
   1                    5                    10                    15  
 tcc ctg agg ctc tcc tgt gca gcc tct gga ttc act ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
                     20                    25                    30  
 ggt atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                     35                    40                    45  
 tca ctt ata aca tat gat gga agg aat aaa tac tac gcc gac tcc gtg 192  
 Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val  
                     50                    55                    60

aag ggc cga ttc acc atc tcc aga gag aat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga act gag gac acg gct gag tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Glu Tyr Tyr Cys  
 85 90 95

gcg aga gac ggg atc gga tac ttt gac tac tgg ggc cag gga atc ctg 336  
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Ile Leu  
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

ctg gtg aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aag tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Lys Ser  
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

cac 675  
 His  
 225

<210> 100

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-20H

<400> 100

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Glu Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Ile Leu  
 100 105 110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Lys Ser  
 145 150 155 160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
225

<210> 101  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (675)

<220>  
 <223> M2-31H

<400> 101  
 cag gtg cag ctg gtg gag tct ggg gga gtc gtg gtc cag cct ggg agg 48  
 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Arg  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg ttc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30  
 ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg 144  
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35	40	45	
gca ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg			192
Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val			
50	55	60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat			240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt			288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg			336
Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
	100	105	110
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg			384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu			
	115	120	125
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc			432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys			
	130	135	140
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca			480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser			
	145	150	155
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc			528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser			
	165	170	175
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc			576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser			
	180	185	190
ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac			624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn			
	195	200	205
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat			672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His			
	210	215	220
cac			675
His			
225			

&lt;210&gt; 102

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;223&gt; M2-31H

&lt;400&gt; 102

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
                   20                  25                  30  
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
                   35                  40                  45  
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
                   50                  55                  60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                  70                  75                  80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                  90                  95  
 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                   100                  105                  110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
                   115                  120                  125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
                   130                  135                  140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
                   145                  150                  155                  160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                   165                  170                  175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
                   180                  185                  190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
                   195                  200                  205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
                   210                  215                  220  
 His  
 225

<210> 103  
 <211> 708  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(708)

<220>  
 <223> M2-32H

<400> 103  
 cag gtg cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
           1                  5                  10                  15

tcc	ctg	aga	ctc	tcc	tgt	gaa	ggc	tct	gga	ttc	atc	ttc	agg	aac	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Gly	Ser	Gly	Phe	Ile	Phe	Arg	Asn	His	
			20					25					30			
cct	ata	cac	tgg	gtt	cgc	cag	gct	cca	gga	aaa	ggg	ctg	gag	tgg	gta	144
Pro	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
tca	gtt	agt	ggg	att	ggg	ggg	gac	aca	tac	tat	gca	gac	tcc	gtg	aag	192
Ser	Val	Ser	Gly	Ile	Gly	Gly	Asp	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	
	50					55					60					
ggc	cga	ttc	tcc	atc	tcc	aga	gac	aat	gcc	aag	aac	tcc	ttg	tat	ctt	240
Gly	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	
	65					70				75					80	
caa	atg	aac	agc	ctg	aga	gcc	gag	gac	atg	gct	gtg	tat	tac	tgt	gca	288
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala	
			85					90						95		
aga	gaa	tat	tac	tat	ggg	tcg	ggg	agt	tat	cgc	gtt	gac	tac	tac	tac	336
Arg	Glu	Tyr	Tyr	Tyr	Gly	Ser	Gly	Ser	Tyr	Arg	Val	Asp	Tyr	Tyr	Tyr	
			100					105					110			
tac	ggg	atg	gac	gtc	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	384
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
		115					120					125				
gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	432
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	
	130					135					140					
agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	480
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	
	145				150					155					160	
ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	528
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
			165					170						175		
ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	576
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
			180					185					190			
ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	624
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
			195				200					205				
tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	672
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
	210					215					220					
aaa	gca	gag	ccc	aaa	tct	cat	cac	cat	cac	cat	cac					708
Lys	Ala	Glu	Pro	Lys	Ser	His	His	His	His	His	His					
	225				230						235					

&lt;210&gt; 104

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<223> M2-32H

<400> 104

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Gly		
1				5					10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Gly	Ser	Gly	Phe	Ile	Phe	Arg	Asn	His		
			20					25					30				
Pro	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
Ser	Val	Ser	Gly	Ile	Gly	Gly	Asp	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys		
	50					55					60						
Gly	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu		
65					70					75					80		
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala		
				85					90					95			
Arg	Glu	Tyr	Tyr	Tyr	Gly	Ser	Gly	Ser	Tyr	Arg	Val	Asp	Tyr	Tyr	Tyr		
			100					105					110				
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
		115					120					125					
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys		
	130					135					140						
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr		
145					150					155					160		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser		
				165					170					175			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser		
			180					185					190				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr		
		195					200					205					
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys		
	210					215					220						
Lys	Ala	Glu	Pro	Lys	Ser	His	His	His	His	His	His						
225					230					235							

<210> 105

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (675)

<220>

<223> M2-33H

675

<210> 106  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-33H

<400> 106

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 107  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (675)

<220>  
 <223> M2-34H

<400> 107

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	agg	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acg	ttc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Tyr	Tyr	
			20					25					30			
ggc	ata	cac	tgg	gtc	cgc	cag	gtt	cca	ggc	aag	gga	cta	gag	tgg	gtg	144
Gly	Ile	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
gta	ctt	ata	tca	tac	gat	gga	agc	aat	aaa	tac	tac	gca	gac	tcc	gtg	192
Val	Leu	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	act	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		
ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
gcg	aga	gac	tgg	atc	ggg	tac	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Trp	Ile	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
		100						105					110			
gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
		115					120					125				
gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
	130					135					140					
ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145					150				155					160		
ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	528
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
				165				170					175			
tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	576
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
		180						185				190				
ctg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	624
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
	195						200					205				
acc	aag	gtg	gac	aag	aaa	gca	gag	ccc	aaa	tct	cat	cac	cat	cac	cat	672

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

cac  
 His  
 225

675

<210> 108  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-34H

<400> 108  
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr  
 20 25 30  
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Val Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
 195 200 205  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
 210 215 220

His  
 225

<210> 109  
 <211> 675  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (675)

<220>  
 <223> M2-35H

<400> 109  
 cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg 48  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg atc agt tac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Tyr Tyr  
 20 25 30

ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg 144  
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gaa ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg 192  
 Glu Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg 336  
 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432  
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624  
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
           195                          200                          205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672  
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His  
           210                          215                          220

cac 675  
 His  
 225

<210> 110  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <223> M2-35H

<400> 110  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
       1                          5                          10                          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Tyr Tyr  
                           20                          25                          30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
           35                          40                          45

Glu Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
       50                          55                          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
       65                          70                          75                          80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                           85                          90                          95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
                           100                          105                          110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
           115                          120                          125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
       130                          135                          140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
       145                          150                          155                          160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
                           165                          170                          175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
           180                          185                          190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
       195                          200                          205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His

210

215

220

His  
225

<210> 111  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Figure 2 Kappa Chain

<400> 111  
tatttccagc ttggtccctc tagagttaac gatatcaacg tttatctaata cagcaagaga 60  
tggaggcttg 70

<210> 112  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Figure 2 Heavy Chain

<400> 112  
tgaggttcct tgaccccaact gcagagtact aggcctctga gctactcagt taggtgattg 60  
agtagccagt 70